

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 07:01:10 ; Search time 509 Seconds

(without alignments)
8953.231 Million cell updates/sec

Title: US-09-939-537-32

Perfect score: 768
Sequence: 1 GCTACGAGAGCCCAATCTT.....GGGCTCTGACGACGATCC 768

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	768	100.0	10	US-09-939-537-32
2	696	90.6	16	US-10-363-427-9
3	695.2	90.5	18	US-10-617-619-13
4	695.2	90.5	18	US-10-617-619-10
5	695	90.5	13	US-10-363-427-15
6	695	90.5	13	US-10-363-427-13
7	695	90.5	16	US-10-363-427-11
8	694.8	90.4	17	US-10-452-646-10
9	694.4	90.4	16	US-10-363-427-1
10	694.4	90.4	1428	US-09-740-002-19
11	694.4	90.4	9	US-09-335-697B-19

12	694.4	90.4	1428	17	US-10-384-356-19
13	694.4	90.4	1428	17	US-10-325-698-19
14	694.4	90.4	1431	9	US-09-758-173-3
15	694.4	90.4	1431	9	US-09-758-173-11
16	694.4	90.4	1431	9	US-09-948-4298-3
17	694.4	90.4	1431	9	US-09-948-4298-11
18	694.4	90.4	1431	13	US-10-124-905-3
19	694.4	90.4	1431	13	US-10-124-905-11
20	694.4	90.4	1431	13	US-10-073-138-2
21	694.4	90.4	1431	13	US-10-073-138-6
22	694.4	90.4	1431	16	US-10-124-807-3
23	694.4	90.4	1431	16	US-10-124-807-11
24	694.4	90.4	1431	16	US-10-124-807-4
25	694.4	90.4	1431	16	US-10-291-532-3
26	694.4	90.4	1437	16	US-10-291-532-11
27	694.4	90.4	1437	9	US-09-948-4298-7
28	694.4	90.4	1437	13	US-10-124-905-7
29	694.4	90.4	1437	13	US-10-073-138-4
30	694.4	90.4	1437	16	US-10-124-807-7
31	694.4	90.4	1437	16	US-10-291-532-7
32	694.4	90.4	1437	16	US-10-363-427-5
33	694.4	90.4	9199	10	US-09-911-697-3
34	694.4	90.4	9209	10	US-09-911-703-3
35	694.4	90.4	9209	10	US-09-905-928-2
36	694.4	90.4	9209	14	US-10-096-964-2
37	694.4	90.4	9209	15	US-10-238-681-3
38	694.4	90.4	9209	17	US-10-411-026-58
39	694.4	90.4	9209	17	US-10-411-026-58
40	694.4	90.4	9209	17	US-10-410-962-58
41	694.4	90.4	9209	17	US-10-411-049-58
42	694.4	90.4	9209	18	US-10-410-930-58
43	694.4	90.4	9209	18	US-10-410-997-58
44	694.4	90.4	9209	18	US-10-411-012-58
45	694.4	90.4	9209	18	US-10-287-994-58

ALIGNMENTS

Sequence 19, Appl
Sequence 19, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 7, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 58, Appl

RESULT 1
US-09-939-537-32
Sequence 32, Application US/09939537
Publication No. US20030138410A1

GENERAL INFORMATION:
APPLICANT: Seed, Brian
Banapur, Babak
Romeo, Charles
Kolanus, Waldemar

TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939, 537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566

FILED DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-939-537-32

Query Match 100.0%; Score 768; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 7,8e-191;
Matches 768; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTAGCAGAGCCCAATCTTGTGACAAACTGACACATGCCGACCGTGCCGACGACCTGA 60
DB 1 GCTAGCAGAGCCCAATCTTGTGACAAACTGACACATGCCGACCGTGCCGACGACCTGA 60
QY 61 ACTCTGGGGGGGACCGCTGAGTCTTCTTCCCCCAAAACCCAGAGACACCTTCATGAT 120
DB 61 ACTCTGGGGGGGACCGCTGAGTCTTCTTCCCCCAAAACCCAGAGACACCTTCATGAT 120
QY 121 CTCCCGGACCCCTGAGGTGACATGCTGTGTGTGACGTGAGCCAGAGACCTTGAGGT 180
DB 121 CTCCCGGACCCCTGAGGTGACATGCTGTGTGTGACGTGAGCCAGAGACCTTGAGGT 180
QY 181 CAAGTTCAACTGTGACGTGACGCGGTGAGGTGATATGCTCAAGCAAAAGCCGCGGGA 240
DB 181 CAAGTTCAACTGTGACGTGACGCGGTGAGGTGATATGCTCAAGCAAAAGCCGCGGGA 240
QY 241 GGAGCAGTACAAACAGACGTACCGGGTGTGTCAGCGTCTTCCAGCAGCAGGACTG 300
DB 241 GGAGCAGTACAAACAGACGTACCGGGTGTGTCAGCGTCTTCCAGCAGCAGGACTG 300
QY 301 GCTGATGCGAAGAGTACAGTGCAGAGTCTCCAAAGACCTCCGACCCCATGCA 360
DB 301 GCTGATGCGAAGAGTACAGTGCAGAGTCTCCAAAGACCTCCGACCCCATGCA 360
QY 361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAACAAGGTGACACCTGCCCC 420
DB 361 GAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAACAAGGTGACACCTGCCCC 420
QY 421 ATCCCGGAGATGAGCTGACCAAGAACAGGTCACTGCTGTGCTTAAAGGCTTCTGA 480
DB 421 ATCCCGGAGATGAGCTGACCAAGAACAGGTCACTGCTGTGCTTAAAGGCTTCTGA 480
QY 481 TCCCAAGGACATGCGCTGTGAGTGGAGCAATGGGACGCGGAGAACATTAAGAC 540
DB 481 TCCCAAGGACATGCGCTGTGAGTGGAGCAATGGGACGCGGAGAACATTAAGAC 540
QY 541 CAGCGCTCCCGTGTGCTGCACTCCGACGGCTCTTCTTCCCTTCAAGCAGCTCACTGGA 600
DB 541 CAGCGCTCCCGTGTGCTGCACTCCGACGGCTCTTCTTCCCTTCAAGCAGCTCACTGGA 600
QY 601 CAAGAGCAGGTGGCAGCAGAGGGGAAAGCTTCTTCATGCTCCGAGTGCATGAGGCTCTGCA 660
DB 601 CAAGAGCAGGTGGCAGCAGAGGGGAAAGCTTCTTCATGCTCCGAGTGCATGAGGCTCTGCA 660
QY 661 CAACCACTACAGCAGAGAAGGCTCTCCCTGTCTCCGGGCTGCAACTGACGAGACTG 720
DB 661 CAACCACTACAGCAGAGAAGGCTCTCCCTGTCTCCGGGCTGCAACTGACGAGACTG 720
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QY 721 TGCTGAGGCCCAAGACCGGGAGCTGACGCGGCTCTGAGACGACGATCC 768
DB 721 TGCTGAGGCCCAAGACCGGGAGCTGACGCGGCTCTGAGACGACGATCC 768

RESULT 2
US-10-363-427-9
Sequence 9, Application US/10363427
Publication No. US20030195338A1
GENERAL INFORMATION:
APPLICANT: Medexgen Inc.
APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
TITLE OF INVENTION: Concatameric Immunoadhesion
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Kopatentin 1.71
SEQ ID NO 9
LENGTH: 1827
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1824)
OTHER INFORMATION: mgTNPRI-TNPRI-IgG
FEATURE:
NAME/KEY: C region
LOCATION: (1126)..(1827)
OTHER INFORMATION: Hinge, CH2, CH3 region
FEATURE:
NAME/KEY: misc signal
LOCATION: (160)..(168)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (433)..(441)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (451)..(459)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (565)..(573)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (574)..(582)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (592)..(600)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (610)..(618)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (925)..(933)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (943)..(951)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: primer_bind
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? LOCATION: (1)..(15)
? OTHER INFORMATION: PCR primer SEQ ID : 25 binding site
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: (545)..(606)
? OTHER INFORMATION: PCR primer SEQ ID : 37(antisense) binding site
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: (559)..(621)
? OTHER INFORMATION: PCR primer SEQ ID : 36 binding site
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: (1108)..(1144)
? OTHER INFORMATION: PCR primer SEQ ID : 26(antisense) binding site
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: (1108)..(1144)
? OTHER INFORMATION: PCR primer SEQ ID : 27 binding site
? FEATURE:
? NAME/KEY: primer_bind
? LOCATION: (1804)..(1827)
? OTHER INFORMATION: PCR primer SEQ ID : 28(antisense) binding site
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: (1)..(60)
? OTHER INFORMATION: signal peptide
? OS-10-363-427-9

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Query Match	90.6%	Score 696	DB 16	Length 1827
Best Local Similarity	100.0%	Pred. No.	5.2e-172	
Matches 696; Conservative	0	Mismatches	0	Gaps 0

4 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCCAACCGTGCCCAAGCACCCTGA

QY	4	AGCAGAGCCCAAACTCTTGTGACAAAATCTACACATGAGCCACCGTGTCCGAGACCTGAACT	63
Db	1125	AGCAGAGCCCAAACTCTTGTGACAAAATCTACACATGAGCCACCGTGTCCGAGACCTGAACT	1188
QY	64	CTGTGGGGGAGACCGTCAAGTCTTCTCTTCCCCCAAAACCCAAAGACACCTTCATGATCTC	123
Db	1185	CCTGGGGGGAGACCGTCAAGTCTTCTCTTCCCCCAAAACCCAAAGACACCTTCATGATCTC	1244
QY	124	CCGGACCCCTTAAGGTCACATATCGTGTGTGTGACGTGAGCCACGAAGACCTTGAAAGTCA	183
Db	1245	CCGGACCCCTTAAGGTCACATATCGTGTGTGTGACGTGAGCCACGAAGACCTTGAAAGTCA	1304
QY	184	GTTCAACTGTATCGTGAACGGCGGTGGAAGTGCATATATGCCAAGACAAAGCCGCGGAGGA	243
Db	1305	GTTCAACTGTATCGTGAACGGCGGTGGAAGTGCATATATGCCAAGACAAAGCCGCGGAGGA	1364
QY	244	GCAGTACAAACAGACGTACCGGGGTGTGACGCTCTCAACCGTCTTGACACAGAACTGCT	303
Db	1365	GCAGTACAAACAGACGTACCGGGGTGTGACGCTCTCAACCGTCTTGACACAGAACTGCT	1422
QY	304	GAATGGCAAGAGATTCAGTGCAGGTCTTCCAAACAAAGCCCTTCCAGCCCCCATGTAGAA	363
Db	1425	GAATGGCAAGAGATTCAGTGCAGGTCTTCCAAACAAAGCCCTTCCAGCCCCCATGTAGAA	1484
QY	364	AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGAGGTATCAACCTGTCCCCATC	423
Db	1485	AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGAGGTATCAACCTGTCCCCATC	1544
QY	424	CCGGGATGAGTGAACCAAGAACCAAGGTGACCTGACTCTGTCAAAAGCTTCTATCC	483
Db	1545	CCGGGATGAGTGAACCAAGAACCAAGGTGACCTGACTCTGTCAAAAGCTTCTATCC	1604
QY	484	CAGGGAATTCGCCCGTGTGAGTGTGGAGAGCAATGGGCAAGCCGAGAACCACTAACAAACAC	543
Db	1605	CAGGGAATTCGCCCGTGTGAGTGTGGAGAGCAATGGGCAAGCCGAGAACCACTAACAAACAC	1664
QY	544	GCCTTCCCGTGTGACTCCGAGACGGCTCTTCTTCTTACAGCAAGCTTCAACGTTGAGACAA	603
Db	1665	GCCTTCCCGTGTGACTCCGAGACGGCTCTTCTTCTTACAGCAAGCTTCAACGTTGAGACAA	1722
QY	604	GAGCAGGTGACAGCAGGGGAAAGTCTTCTCATGCTCCGTGATGATGAGGCTTGTACAA	663

Db 1725 GAGCAGGTGGAGCAGGGGAGACGTCTTCTATAGCTCCGTATGCAATAGGCTCTGCACAA 1784

Qy 664 CCACCTACACGCGAAGAGCCTCTCCCTGTCTCCGGG 699

Db 1785 CCACCTACACGCGAAGAGCCTCTCCCTGTCTCCGGG 1820

RESULT 3

```

: Sequence 13, Application US/10617619
: Publication No. US20040110929A1
: GENERAL INFORMATION:
: APPLICANT: Nicolaisen, Else M
: APPLICANT: Bjorn, Soren E
: APPLICANT: Jorgensen, Anker S
: TITLE OF INVENTION: 1P Binding Compound
: FILE REFERENCE: 6455.200-US
: CURRENT APPLICATION NUMBER: US/10/617, 619
: CURRENT FILING DATE: 2003-07-11
: PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 0109
: PRIOR FILING DATE: 2002-07-12
: PRIOR APPLICATION NUMBER: US 60/404,568
: PRIOR FILING DATE: 2002-08-19
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 13
: LENGTH: 7427
: TYPE: DNA
: ORGANISM: Artificial
: FEATURES:
: OTHER INFORMATION: Synthetic
: US-10-617-619-13

```

Query Match	90.5%	Score 695.2	DB 18	length 7427
Best Local Similarly	98.2%	Pred. NC 9.2e-172		
Matches 703, Conservative	0	Mismatches 13	Indels 0	Gaps 0

OY	5	GCAGAGCCCAATCTTGAGCAAAAATCAACATGCCACCGGTGCCGAGCACTGAAATTC	64
Db	1349	GCAGAGCCCAATCTTGAGCAAAAATCAACATGCCACCGGTGCCGAGCACTGAAATTC	1408
OY	65	CTGGGGGGGACCGTAGCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCC	124
Db	1409	CTGGGGGGGACCGTAGCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTTC	1466
OY	125	CGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCAGAGACCTTGAGGTCAAG	184
Db	1469	CGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCAGAGACCTTGAGGTCAAG	1522
OY	185	TTCAACTGGTACGTGACGGCGTGGAGGTGATATATGCCAAGACAAAGCCGGGGAGAG	244
Db	1529	TTCAACTGGTACGTGACGGCGTGGAGGTGATATATGCCAAGACAAAGCCGGGGAGAG	1588
OY	245	CAGTACCAACAGCAAGTACCGGGTGGTCAAGCTCTTCAACCGTCCGTGACACAGACTGGGTG	304
Db	1589	CAGTACCAACAGCAAGTACCGGTGGTCAAGCTCTTCAACCGTCCGTGACACAGACTGGGTG	1648
OY	305	AATGGAAGAGGTACAAGTGCAGAGTCTCCCAAAGAGCCCTCCAGCCCCCATCGAGAA	364
Db	1649	AATGGAAGAGGTACAAGTGCAGAGTCTTCCCAAAGAGCCCTCCAGCCCCCATCGAGAA	1708
OY	365	ACCATCTTCAAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCTGCCCCCATCC	424
Db	1709	ACCATCTTCAAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCTGCCCCCATCC	1768
OY	425	CGGATGAGCTGACCAAGAACCAAGTCAAGCTTGAACCTGCTGGTCAAAAGCTTCTATATCC	484
Db	1769	CGGATGAGCTGACCAAGAACCAAGTCAAGCTTGAACCTGCTGGTCAAAAGCTTCTATATCC	1828
OY	485	AGGCAACATCCCGGTGGAGTGGGAGAACGAATGGGACCGGAGAACATCTACAAGCCAG	544
Db	1829	AGGCAACATCCCGGTGGAGTGGGAGAACGAATGGGACCGGAGAACATCTACAAGCCAG	1888

```

Db      1835  CGGAGTGAAGCTGACCAAGAAACAGGTCAAGCTGACCTGCTGTGTAAAGCTTTATCCC
Oy      485   AGGACATGTCCTGTGAGTGGAGAGCAATGGGACGCGGAAACAATTACAAGACACG
Db      1895  AGGAGATCTGCGGTGAGTGGAGAGCAATGGGACGCGGAAACAATTACAAGACACG
Oy      545   CCTCCCGTGTGGAATCCGACGGGCTCCTTTCTCTTACAGCAAGCTACCGTGGACAAG
Db      1955  CCTCCCGTGTGGAATCCGACGGGCTCCTTTCTCTTACAGCAAGCTACCGTGGACAAG
Oy      605   AGCAGTGGCAGCAGGGGAAACGTCTTCTCAATGCTCCGTGATGATGAGGCTTGCAAC
Db      2015  AGCAGTGGCAGCAGGGGAAACGTCTTCTCAATGCTCCGTGATGATGAGGCTTGCAAC
Oy      665  CACTACACGCAAGAAAGCCTCTCCTGTCTCGGGGCTGCAACTGACGAGACCTG
Db      2075  CACTACACGCAAGAAAGCCTCTCCTGTCTCGGGGTAATGAAAGGCGCAATTCTG
RESULT 5
US-10-363-427-15
/ Sequence 15, Application US/10363427
/ Publication No. US20030195358A1
/ GENERAL INFORMATION:
/ APPLICANT: Medexen Inc.
/ APPLICANT: CHUNG, Yong Hoon
/ APPLICANT: HAN, Ji Woong
/ APPLICANT: LEE, Hye Ja
/ APPLICANT: CHOI, Eun Yong
/ APPLICANT: KIM, Jin Mi
/ APPLICANT: YIM, Soo Bin
/ TITLE OF INVENTION: Concatametric Immunoaddhesion
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/363,427
/ CURRENT FILING DATE: 2003-02-28
/ NUMBER OF SEQ ID NOS: 52
/ SOFTWARE: Kopacencin 1.71
/ SEQ ID NO 15
/ LENGTH: 1134
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1131)
/ OTHER INFORMATION: CTLA4-IgG
/ FEATURE:
/ NAME/KEY: C.region
/ LOCATION: (433)..(1134)
/ OTHER INFORMATION: Hinge, CH2, CH3 region
/ FEATURE:
/ NAME/KEY: misc_signal
/ LOCATION: (289)..(297)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: misc_signal
/ LOCATION: (385)..(393)
/ OTHER INFORMATION: N-linked glycosylation site
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (1)..(15)
/ OTHER INFORMATION: PCR primer SEQ ID : 43 binding site
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (409)..(438)
/ OTHER INFORMATION: PCR primer SEQ ID : 44(antisense) binding site
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (430)..(453)
/ OTHER INFORMATION: PCR primer SEQ ID : 42 binding site
/ NAME/KEY: primer_bind
/ LOCATION: (1111)..(1134)

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; OTHER INFORMATION: PCR primer SEQ ID : 28(antisense) binding site
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(63)
; OTHER INFORMATION: signal peptide
US-10-363-427-15

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Query Match          90.5%; Score 695; DB 16; Length 1134;
Best Local Similarity 100.0%; Pred. No. 9.3e-172;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 GCAGAGCCCAAACTTGTGACAAACTCAGACATGCCACCGTGCCAGACCTGAATCTC 64
DB 433 GCAGAGCCCAAACTTGTGACAAACTCAGACATGCCACCGTGCCAGACCTGAATCTC 492
QY 65 CTGGGGGGGACCGGTCACTCTCTCTTCCCGCCCAAAACCGAAGACACCTCATGATCTCC 124
DB 493 CTGGGGGGGACCGGTCACTCTCTCTTCCCGCCCAAAACCGAAGACACCTCATGATCTCC 552
QY 125 CGGACCCCTGAGGTCACTGCGTGTGTGAGCGTGAAGCCAGAGACCTGAGGTCAAG 184
DB 553 CGGACCCCTGAGGTCACTGCGTGTGTGAGCGTGAAGCCAGAGACCTGAGGTCAAG 612
QY 185 TTCAACTGTGACGTGACCGCGTGTGAGGTGATATGCAAGACAAAGCCGCGGAGAG 244
DB 613 TTCAACTGTGACGTGACCGCGTGTGAGGTGATATGCAAGACAAAGCCGCGGAGAG 672
QY 245 CAGTACACAGCAGTCATCCGGGTGTGACGCTCTCAACCGTCTCTGACACGACTGCTG 304
DB 673 CAGTACACAGCAGTCATCCGGGTGTGACGCTCTCAACCGTCTCTGACACGACTGCTG 732
QY 305 AATGGACAGGAGTACAGTGAAGTCTCCAAACAAAGCCCTCCAGCCCGCCATGAGAAA 364
DB 733 AATGGACAGGAGTACAGTGAAGTCTCCAAACAAAGCCCTCCAGCCCGCCATGAGAAA 792
QY 365 ACCATCTCCAAAGCCAAAGGCGACCCCGAAGAACCAAGGTGTATCAACCTGCCCCATCC 424
DB 793 ACCATCTCCAAAGCCAAAGGCGACCCCGAAGAACCAAGGTGTATCAACCTGCCCCATCC 852
QY 425 CGGAGTAGAGTGAACCAAGAACCAAGGTGACCTGCTGTGTCAAAGGCTTCTATCCC 484
DB 853 CGGAGTAGAGTGAACCAAGAACCAAGGTGACCTGCTGTGTCAAAGGCTTCTATCCC 912
QY 485 AGGCATCAGCGCGTGAAGTGAAGAGCAATGGGACGCGGAGAACCACTACAGACCAAG 544
DB 913 AGGCATCAGCGCGTGAAGTGAAGAGCAATGGGACGCGGAGAACCACTACAGACCAAG 972
QY 545 CCTCCGCTGTGACTCCGACGCGCTCTTCTCTCTTACAGCAAGCTCAACCGTGAACAG 604
DB 973 CCTCCGCTGTGACTCCGACGCGCTCTTCTCTCTTACAGCAAGCTCAACCGTGAACAG 1032
QY 605 AGCAGGTGCGACAGAGGGGAAAGTCTTCTCATGCTCCGTATGATAGAGCTTGACACAC 664
DB 1033 AGCAGGTGCGACAGAGGGGAAAGTCTTCTCATGCTCCGTATGATAGAGCTTGACACAC 1092
QY 665 CACTACACGAGAGAGCGCTCTCCCTGTCTCCCGGG 699
DB 1093 CACTACACGAGAGAGCGCTCTCCCTGTCTCCCGGG 1127

```

```

RESULT 6
US-10-363-427-13
; Sequence 13, Application US/10363427
; Publication No. US20030195338A1
; GENERAL INFORMATION:
; APPLICANT: Medexgen Inc.
; APPLICANT: CHUNG, Yong Hoon
; APPLICANT: HAN, Ji Moong
; APPLICANT: LEE, Hye Ja
; APPLICANT: CHOI, Eun Yong
; APPLICANT: KIM, Jin Mi
; APPLICANT: YIM, Soo Bin
; TITLE OF INVENTION: Concatameric Immunoadhesion

```

```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO: 13
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1311)
; OTHER INFORMATION: CD2-19G
; FEATURE:
; NAME/KEY: C region
; LOCATION: (613)..(1314)
; OTHER INFORMATION: Hinge, CH2, CH3 region
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (421)..(429)
; OTHER INFORMATION: N-linked glycosylation site
; FEATURE:
; NAME/KEY: misc_signal
; LOCATION: (448)..(456)
; OTHER INFORMATION: N-linked glycosylation site
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(27)
; OTHER INFORMATION: PCR primer SEQ ID : 40 binding site
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (589)..(618)
; OTHER INFORMATION: PCR primer SEQ ID : 41(antisense) binding site
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (611)..(633)
; OTHER INFORMATION: PCR primer SEQ ID : 42 binding site
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1292)..(1314)
; OTHER INFORMATION: PCR primer SEQ ID : 28(antisense) binding site
; NAME/KEY: sig_peptide
; LOCATION: (1)..(72)
; OTHER INFORMATION: signal peptide
US-10-363-427-13

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Query Match          90.5%; Score 695; DB 16; Length 1314;
Best Local Similarity 100.0%; Pred. No. 9.4e-172;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 GCAGAGCCCAAACTTGTGACAAACTCAGACATGCCACCGTGCCAGACCTGAATCTC 64
DB 613 GCAGAGCCCAAACTTGTGACAAACTCAGACATGCCACCGTGCCAGACCTGAATCTC 672
QY 65 CTGGGGGGGACCGGTCACTCTCTCTTCCCGCCCAAAACCGAAGACACCTCATGATCTCC 124
DB 673 CTGGGGGGGACCGGTCACTCTCTCTTCCCGCCCAAAACCGAAGACACCTCATGATCTCC 732
QY 125 CGGACCCCTGAGGTCACTGCGTGTGTGAGCGTGAAGCCAGAGACCTTGAAGTCAAG 184
DB 733 CGGACCCCTGAGGTCACTGCGTGTGTGAGCGTGAAGCCAGAGACCTTGAAGTCAAG 792
QY 185 TTCAACTGTGACGTGACCGCGTGTGAGGTGATATGCAAGACAAAGCCGCGGAGAG 244
DB 793 TTCAACTGTGACGTGACCGCGTGTGAGGTGATATGCAAGACAAAGCCGCGGAGAG 852
QY 245 CAGTACACAGCAGTCATCCGGGTGTGACGCTCTCAACCGTCTCTGACACGACTGCTG 304

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```
Db 853 CAGTACACAGCAGTACCGGGTGTGACGCTCTCACCGTCTGACCAAGAGTGGCTG 912
Qy 305 AATGGCAAGAGTACAGTGCAGAGTCTTCCAAAGCCCTCCCGCCCATGAGAAA 364
Db 913 AATGGCAAGAGTACAGTGCAGAGTCTTCCAAAGCCCTCCCGCCCATGAGAAA 972
Qy 365 ACCATCTCCAAAGCCCAAGGGGAGCCCGAGAACCAAGGTGACACCTGGCCCCATCC 424
Db 973 ACCATCTCCAAAGCCCAAGGGGAGCCCGAGAACCAAGGTGACACCTGGCCCCATCC 1032
Qy 425 CGGGATGAGCTGACCAAGAACCAAGTACCTGACCTGCTTGTCAAAGCTTTCTATCC 484
Db 1033 CGGGATGAGCTGACCAAGAACCAAGTACCTGACCTGCTTGTCAAAGCTTTCTATCC 1092
Qy 485 AGCGACATGCGCTGAGTGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACCAAG 544
Db 1093 AGCGACATGCGCTGAGTGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACCAAG 1152
Qy 545 CTTCCCGTGTGAGCTCCGACGCGCTCTTCTCTTACAGCAAGCTCACCGTGCAGAG 604
Db 1153 CTTCCCGTGTGAGCTCCGACGCGCTCTTCTCTTACAGCAAGCTCACCGTGCAGAG 1212
Qy 605 AGCAGGTGGACGAGGGGAAAGCTTTCTCATGCTCGTGAATGATGAGGCTTGACAAAC 664
Db 1213 AGCAGGTGGACGAGGGGAAAGCTTTCTCATGCTCGTGAATGAGGCTTGACAAAC 1272
Qy 665 CACTACACGAGAAAGAGCTCTCCCTGCTCCGGG 699
Db 1273 CACTACACGAGAAAGAGCTCTCCCTGCTCCGGG 1307
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RESULT 7
US-10-363-427-11

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Sequence 11, Application US/10363427
Publication No. US20030195338A1
GENERAL INFORMATION:
APPLICANT: Medexgen Inc.
APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
TITLE OF INVENTION: Concatameric Immunoadhesion
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Kopatentin 1.71
SEQ ID NO 11
LENGTH: 1980
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1977)
OTHER INFORMATION: mgTmFR2-TmFR2-IgG
FEATURE:
NAME/KEY: C_region
LOCATION: (1279)..(1980)
OTHER INFORMATION: Hinge, CH2, CH3 region
FEATURE:
NAME/KEY: misc_signal
LOCATION: (511)..(519)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc_signal
LOCATION: (577)..(585)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc_signal
LOCATION: (595)..(603)
OTHER INFORMATION: N-linked glycosylation site
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FEATURE:
NAME/KEY: misc_signal
LOCATION: (616)..(624)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc_signal
LOCATION: (1018)..(1026)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc_signal
LOCATION: (1084)..(1092)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (1)..(15)
OTHER INFORMATION: PCR primer SEQ ID : 29 binding site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (586)..(627)
OTHER INFORMATION: PCR primer SEQ ID : 39(antisense) binding site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (586)..(630)
OTHER INFORMATION: PCR primer SEQ ID : 38 binding site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (1261)..(1296)
OTHER INFORMATION: PCR primer SEQ ID : 30(antisense) binding site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (1261)..(1296)
OTHER INFORMATION: PCR primer SEQ ID : 31 binding site
FEATURE:
NAME/KEY: primer_bind
LOCATION: (1957)..(1980)
OTHER INFORMATION: PCR primer SEQ ID : 28(antisense) binding site
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(66)
OTHER INFORMATION: signal peptide
US-10-363-427-11

Query Match 90.5%; Score 695; DB 16; Length 1980;
Best Local Similarity 100.0%; Pred. No. 9.6e-172;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCAGAGCCCAATCTTGTGACAAACTCAACATGCCCCCGTGGCCAGCCTGAATC 64
Db 1279 GCAGAGCCCAATCTTGTGACAAACTCAACATGCCCCCGTGGCCAGCCTGAATC 1338
Qy 65 CTGGGGGAGACCTGCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCC 124
Db 1339 CTGGGGGAGACCTGCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCC 1398
Qy 125 CGACCCCTGAGGTGACATGCGTGTGTGAGCTGAGCGCAAGAACCTTGAAGTCAAG 184
Db 1399 CGACCCCTGAGGTGACATGCGTGTGTGAGCTGAGCGCAAGAACCTTGAAGTCAAG 1458
Qy 185 TTCAACTGTGACGTGAGCGCGCGTGGAGGTGCATATAGCCAAAGCGCGGAGAG 244
Db 1459 TTCAACTGTGACGTGAGCGCGCGTGGAGGTGCATATAGCCAAAGCGCGGAGAG 1518
Qy 245 CAGTACACAGCAGTACCGGGTGTGACGCTCTTCAACGCTCTGCAACGAGACTGGCTG 304
Db 1519 CAGTACACAGCAGTACCGGGTGTGACGCTCTTCAACGCTCTGCAACGAGACTGGCTG 1578
Qy 305 AATGGCAAGAGTACAGTGCAGAGTCTTCCAAAGCCCTCCCGCCCATGAGAAA 364
Db 1579 AATGGCAAGAGTACAGTGCAGAGTCTTCCAAAGCCCTCCCGCCCATGAGAAA 1638
Qy 365 ACCATCTCCAAAGCCCAAGGGGAGCCCGAGAACCAAGGTGACACCTGGCCCCATCC 424
Db 1639 ACCATCTCCAAAGCCCAAGGGGAGCCCGAGAACCAAGGTGACACCTGGCCCCATCC 1698
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QY 425 CCGGATGAGCTGACCAAGAACAGAGTCAAGCTGAGCTGCTCAAGAGGCTTCTATCCC 484
DB 1699 CCGGATGAGCTGACCAAGAACAGAGTCAAGCTGAGCTGCTCAAGAGGCTTCTATCCC 1758
QY 485 AGGACATCGCCGTGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACCAAG 544
DB 1759 AGGACATCGCCGTGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACCAAG 1818
QY 545 CCGCCCGGTGAGCTCCGAGCGGCTCTTCTCTCAAGCAAGCTCAACCTGAGAACAG 604
DB 1819 CCGCCCGGTGAGCTCCGAGCGGCTCTTCTCTCAAGCAAGCTCAACCTGAGAACAG 1878
QY 605 AGCAGGTGGAGAGGAGGAGAACTCTTCTCATGCTCCGTGATGATGAGGCTTGACAAAC 664
DB 1879 AGCAGGTGGAGAGGAGGAGAACTCTTCTCATGCTCCGTGATGATGAGGCTTGACAAAC 1938
QY 665 CACTACACGCAAGAGAGCTCTCCCTGCTCCGAG 699
DB 1939 CACTACACGCAAGAGAGCTCTCCCTGCTCCGAG 1973

RESULT 8
US-10-452-646-10
Sequence 10, Application US/10452646
Publication No. US20040018593A1
GENERAL INFORMATION:
APPLICANT: Carton, Jill M.
APPLICANT: Staquet, Kimberly C.
APPLICANT: Scallion, Bernard J.
APPLICANT: Jili, Giles-Komar
TITLE OF INVENTION: ANTI-RELP FUSION ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0296 NP
CURRENT APPLICATION NUMBER: US/10/452,646
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 60/385,305
PRIOR FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 1104
TYPE: DNA
ORGANISM: homo sapiens
US-10-452-646-10

Query Match 90.5%; Score 694.8; DB 17; Length 1104;
Best Local Similarity 99.7%; Pred. No. 1e-171;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CTAGCAGAGCCCAAAATCTTGTGACAAACACACATGCCCCGAGCCGAGACCTGAA 61
DB 400 CTAACGAGAGCCCAAAATCTTGTGACAAACACACATGCCCCGAGCCGAGACCTGAA 459
QY 62 CTCCTGGGGGAGCCGTCACTCTCTTCTCCCAAAACCAAGACACCTCATGATC 121
DB 460 CTCCTGGGGGAGCCGTCACTCTCTTCTCCCAAAACCAAGACACCTCATGATC 519
QY 122 TCCCGGACCCCTGAGTCAATGCGTGTGTGTGAGTGAAGCAAGAGCCCTGAGGTC 181
DB 520 TCCCGGACCCCTGAGTCAATGCGTGTGTGTGAGTGAAGCAAGAGCCCTGAGGTC 579
QY 182 AAGTTCACTGTAGCTGAGCGGCGTGGAGGTGATTAATGCAAGACCAAGAGCCGCGGAG 241
DB 580 AAGTTCACTGTAGCTGAGCGGCGTGGAGGTGATTAATGCAAGAGAGCCGCGGAG 639
QY 242 GAGCAGTACAAAGCAAGTACCGGGTGTGAGGCTCTCAACCGTCTGCAAGACTGG 301
DB 640 GAGCAGTACAAAGCAAGTACCGGGTGTGAGGCTCTCAACCGTCTGCAAGACTGG 659
QY 302 CTGAATGGCAGAGAGTACAGTGAAGTCTCAACCAAGCCCTCCAGCCCAATGAG 361
DB 700 CTGAATGGCAGAGAGTACAGTGAAGTCTCAACCAAGCCCTCCAGCCCAATGAG 759

QY 362 AAAACATCTCCAAAGCCAAAGGAGAGCCCGAGAAACAAGGTGTACACCTTCCGCCCA 421
DB 760 AAAACATCTCCAAAGCCAAAGGAGAGCCCGAGAAACAAGGTGTACACCTTCCGCCCA 819
QY 422 TCCCGGATGAGCTGACCAAGAACAGAGTCAAGCTGAGCTGCTGCTCAAGGCTTCTAT 481
DB 820 TCCCGGATGAGCTGACCAAGAACAGAGTCAAGCTGAGCTGCTGCTCAAGGCTTCTAT 879
QY 482 CCGAGGACATGCGCCGTGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACC 541
DB 880 CCGAGGACATGCGCCGTGAGTGGGAGAGCAATGGGAGCCGGAGAACAACTACAAGACC 939
QY 542 AGCCTCCCGGTGAGCTCCGAGCGGCTCTTCTCTCAAGCAAGCTCAACCTGAGAC 601
DB 940 AGCCTCCCGGTGAGCTCCGAGCGGCTCTTCTCTCAAGCAAGCTCAACCTGAGAC 999
QY 602 AAGAGAGGTGGAGAGGAGGAGAACTCTTCTCATGCTCCGTGATGATGAGGCTTGAC 661
DB 1000 AAGAGAGGTGGAGAGGAGGAGAACTCTTCTCATGCTCCGTGATGATGAGGCTTGAC 1059
QY 662 AACCACTACACGCAAGAGAGCTCTCCCTGCTCCGAG 699
DB 1060 AACCACTACACGCAAGAGAGCTCTCCCTGCTCCGAG 1097

RESULT 9
US-10-363-427-1
Sequence 1, Application US/10363427
Publication No. US20030195338A1
GENERAL INFORMATION:
APPLICANT: Medexgen Inc.
APPLICANT: Chung, Yong Hoon
APPLICANT: Han, Ji Woong
APPLICANT: Lee, Hye Ja
APPLICANT: Choi, Eun Yong
APPLICANT: Kim, Jin Mi
APPLICANT: Yim, Soo Bin
TITLE OF INVENTION: Concatametric Immunoadhesion
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
LENGTH: 1335
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1332)
OTHER INFORMATION: TNFR1-IgG
FEATURE:
NAME/KEY: C_region
LOCATION: (634)..(1335)
OTHER INFORMATION: Hinge, CH2, CH3 region
FEATURE:
NAME/KEY: misc signal
LOCATION: (160)..(168)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (433)..(441)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: misc signal
LOCATION: (451)..(459)
OTHER INFORMATION: N-linked glycosylation site
FEATURE:
NAME/KEY: primer bind
LOCATION: (1)..(15)
OTHER INFORMATION: PCR primer SEQ ID : 25 binding site
FEATURE:
NAME/KEY: primer_bind

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/ LOCATION: (616)..(652)
/ OTHER INFORMATION: PCR primer SEQ ID : 26(antisense) binding site
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (616)..(651)
/ OTHER INFORMATION: PCR primer SEQ ID : 27 binding site
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (1312)..(1335)
/ OTHER INFORMATION: PCR primer SEQ ID : 28(antisense) binding site
/ FEATURE:
/ NAME/KEY: sig peptide
/ LOCATION: (1)..(60)
/ OTHER INFORMATION: signal peptide
US-10-363-427-1
```

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Query Match          90.4%; Score 694.4; DB 16; Length 1335;
Best Local Similarity 99.9%; Pred. No. 1.3e-171; Indels 0; Gaps 0;
Matches 695; Conservative 0; Mismatches 1;
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```
QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAGATGCCCGTGGCCAGCATCTGAAC 63
DB AGCAGAGCCCAATCTTGTGACAAACTCAGATGCCCGTGGCCAGCATCTGAAC 692
QY 64 CTTGGGGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCCAGAGACCTCTGATCTC 123
DB 693 CTTGGGGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCCAGAGACCTCTGATCTC 752
QY 124 CCGGACCCCTGAGGTCAATGCGGTGTGTGAGAGTGAAGCAGAAAGCCTGAGTCAA 183
DB 753 CCGGACCCCTGAGGTCAATGCGGTGTGTGAGAGTGAAGCAGAAAGCCTGAGTCAA 812
QY 184 GTTCAACTGTGACGTGACGCGGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 243
DB 813 GTTCAACTGTGACGTGACGCGGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 872
QY 244 GCAGTACAAACGACGTCACCGGTGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 303
DB 873 GCAGTACAAACGACGTCACCGGTGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 932
QY 304 GAATGGCAAGAGTACAGAGTCCAAAGTCTCCAAAGACCTTCCAGCCCTCATGAGAA 363
DB 933 GAATGGCAAGAGTACAGAGTCCAAAGTCTCCAAAGACCTTCCAGCCCTCATGAGAA 992
QY 364 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCCATC 423
DB 993 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCCATC 1052
QY 424 CCGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCTGCTCAAAAGCTTCTATCC 483
DB 1053 CCGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCTGCTCAAAAGCTTCTATCC 1112
QY 484 CAGCGACATCGCGGTGTGAGTGGAGAGCAATGGGCAAGCCGGAGAACCACTACAAAGCAC 543
DB 1113 CAGCGACATCGCGGTGTGAGTGGAGAGCAATGGGCAAGCCGGAGAACCACTACAAAGCAC 1172
QY 544 GCCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTCTTACAGAGGCTCAACGCTGAGCAA 603
DB 1173 GCCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTCTTACAGAGGCTCAACGCTGAGCAA 1232
QY 604 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGATGAGAGCTTGCACAA 663
DB 1233 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGATGAGAGCTTGCACAA 1292
QY 664 CCACTACACGCAAGAGAGCTTCTCTGCTCTCGGG 699
DB 1293 CCACTACACGCAAGAGAGCTTCTCTGCTCTCGGG 1328
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RESULT 10
US-09-740-002-19
; Sequence 19, Application US/09740002
; Patent No. US20020001798A1
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```
/ GENERAL INFORMATION:
/ APPLICANT: BRAMS, PETER
/ APPLICANT: MORROW, PHILLIP
/ TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
/ TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
/ TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
/ FILE REFERENCE: 037003-025759
/ CURRENT APPLICATION NUMBER: US/09/740,002
/ CURRENT FILING DATE: 2000-12-20
/ PRIOR APPLICATION NUMBER: 09/335,697
/ PRIOR FILING DATE: 1999-06-18
/ PRIOR APPLICATION NUMBER: 08/488,376
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 1428
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1425)
US-09-740-002-19
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Query Match          90.4%; Score 694.4; DB 9; Length 1428;
Best Local Similarity 99.9%; Pred. No. 1.4e-171; Indels 0; Gaps 0;
Matches 695; Conservative 0; Mismatches 1;
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```
QY 4 AGCAGAGCCCAATCTTGTGACAAACTCAGATGCCCGTGGCCAGCATCTGAAC 63
DB 726 AGCAGAGCCCAATCTTGTGACAAACTCAGATGCCCGTGGCCAGCATCTGAAC 785
QY 64 CTTGGGGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCCAGAGACCTCTGATCTC 123
DB 786 CTTGGGGGGACCGTCACTCTTCTCTTCCCTCCCAAAACCCAGAGACCTCTGATCTC 845
QY 124 CCGGACCCCTGAGGTCAATGCGGTGTGTGAGAGTGAAGCAGAAAGCCTGAGTCAA 183
DB 846 CCGGACCCCTGAGGTCAATGCGGTGTGTGAGAGTGAAGCAGAAAGCCTGAGTCAA 905
QY 184 GTTCAACTGTGACGTGACGCGGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 243
DB 846 GTTCAACTGTGACGTGACGCGGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 905
QY 244 GCAGTACAAACGACGTCACCGGTGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 303
DB 906 GCAGTACAAACGACGTCACCGGTGTGTGAGTGCATTAATGCCAAGCAAAAGCCGGAGGA 965
QY 304 GAATGGCAAGAGTACAGAGTCCAAAGTCTCCAAAGACCTTCCAGCCCTCATGAGAA 363
DB 1026 GAATGGCAAGAGTACAGAGTCCAAAGTCTCCAAAGACCTTCCAGCCCTCATGAGAA 1085
QY 364 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCCATC 423
DB 1086 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCCATC 1145
QY 424 CCGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCTGCTCAAAAGCTTCTATCC 483
DB 1146 CCGGATGAGCTGACCAAGAACAGGTACGCTGACCTGCTGCTCAAAAGCTTCTATCC 1205
QY 484 CAGCGACATCGCGGTGTGAGTGGAGAGCAATGGGCAAGCCGGAGAACCACTACAAAGCAC 543
DB 1206 CAGCGACATCGCGGTGTGAGTGGAGAGCAATGGGCAAGCCGGAGAACCACTACAAAGCAC 1265
QY 544 GCCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTTCTTACAGAGGCTCAACGCTGAGCAA 603
DB 1266 GCCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTTCTTACAGAGGCTCAACGCTGAGCAA 1325
QY 604 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGATGAGAGCTTGCACAA 663
DB 1326 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGATGAGAGCTTGCACAA 1385
QY 664 CCACTACACGCAAGAGAGCTTCTCTGCTCTCGGG 699
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Db 1386 CCACTACAGCGAAGAGCCTCTCCCTGTCTCCGGG 1421

RESULT 11
US-09-335-697B-19
Sequence 19, Application US/09335697B
Publication No. US20020081723A1
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaïma Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335.697B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/770,057
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1428
US-09-335-697B-19
Query Match 90.4%; Score 694.4; DB 9; Length 1428;
Best Local Similarity 99.9%; Pred. No. 1,4e-171;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAATCTCACATGCGCCACCGTCCAGCAGCCTGAAT 63
DB 726 AGCAGAGCCCAATCTTGTGACAAATCTCACATGCGCCACCGTCCAGCAGCCTGAAT 785
QY 64 CCGGAGGAGGAGCGTCACTCTCTCTCCGCCCAAAACCAAGAGCAGCCTCATGATCTC 123
DB 786 CCGGAGGAGGAGCGTCACTCTCTCTCTCCGCCCAAAACCAAGAGCAGCCTCATGATCTC 845
QY 124 CCGGAGCCTCTGAGTGCATGCGTGTGTGTGAGCAGTGAAGCAGCAAGCCTTGAGTCAA 183
DB 846 CCGGAGCCTCTGAGTGCATGCGTGTGTGTGAGCAGTGAAGCAGCAAGCCTTGAGTCAA 905

QY 184 GTTCAACTGTAGCTGAGCAGCGCTGTGAGTGTGATTAATGCCAAGCAAAAGCCGGAGAGA 243
DB 906 GTTCAACTGTAGCTGAGCAGCGCTGTGAGTGTGATTAATGCCAAGCAAAAGCCGGAGAGA 965
QY 244 GCACTACACAGCAGCAGTACCGGAGTGTGAGCTCTCTCAACCGTCTGACAGAGATGGCT 303
DB 966 GCACTACACAGCAGCAGTACCGGAGTGTGAGCTCTCTCAACCGTCTGACAGAGATGGCT 1025
QY 304 GAATGCAAGAGATTAACAAGTGCAGAGCTCTCAACAAAGCCCTCCAGCCCTCCAGAGAA 363
DB 1026 GAATGCAAGAGATTAACAAGTGCAGAGCTCTCAACAAAGCCCTCCAGCCCTCCAGAGAA 1085
QY 364 AACCATCTCCAAAGCCAAAGGAGAGCCCGGAGAACCAAGTGTATCAACCTGCCCCATC 423
DB 1086 AACCATCTCCAAAGCCAAAGGAGAGCCCGGAGAACCAAGTGTATCAACCTGCCCCATC 1145
QY 424 CCGGAGTACCTGACCAAGAACAGGTCAGCTGACCTGCTGCTGCTCAAGGCTTTATTC 483
DB 1146 CCGGAGTACCTGACCAAGAACAGGTCAGCTGACCTGCTGCTGCTCAAGGCTTTATTC 1205
QY 484 CAGCGACATGCGCTGTGAGTGTGAGAGCAATGAGGAGCCGAGAGAACCACTACAAAGCCAC 543
DB 1206 CAGCGACATGCGCTGTGAGTGTGAGAGCAATGAGGAGCCGAGAGAACCACTACAAAGCCAC 1265
QY 544 GCCTCCCGTCTGAGCTCCGAGCGCTCTCTCTCTCTACAGCAAGCTCACCGTGAACA 603
DB 1266 GCCTCCCGTCTGAGCTCCGAGCGCTCTCTCTCTCTACAGCAAGCTCACCGTGAACA 1325
QY 604 GAGCAGGTGACAGCAGGAGAACGTTCTTCATGCTCTGATGATGATGATGATGATGATGAT 663
DB 1326 GAGCAGGTGACAGCAGGAGAACGTTCTTCATGCTCTGATGATGATGATGATGATGATGAT 1385
QY 664 CCACTACAGCGAAGAGCCTCTCCCTGTCTCCGGG 699
DB 1386 CCACTACAGCGAAGAGCCTCTCCCTGTCTCCGGG 1421

RESULT 12
US-10-384-356-19
Sequence 19, Application US/10384356
Publication No. US20040005323A1
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
CHAMAT, Soulaïma Salim
PAN, Li-Zhen
WALSH, Edward E.
HEARD, Cheryl Janne
NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/384,356
FILING DATE: 10-Mar-2003
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1428
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-384-356-19

Query Match 90.4%; Score 694.4; DB 17; Length 1428;
Best Local Similarity 99.9%; Pred. No. 1.4e-171;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 AGCAGAGCCCAATCTTGTCACAAACTCACATGCCCACCTGCGCAGACCTGAAC 63
DB 726 AGCAGAGCCCAATCTTGTCACAAACTCACATGCCCACCTGCGCAGACCTGAAC 785
QY 64 CTTGGGGGGACCGTACGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 123
DB 786 CTTGGGGGGACCGTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 845
QY 124 CCGGACCCCTGAGGTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 183
DB 846 CCGGACCCCTGAGGTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 905
QY 184 GTTCAACTGTGTCGT 243
DB 906 GTTCAACTGTGTCGT 965
QY 244 GCAGTACAAAGAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 303
DB 966 GCAGTACAAAGAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1025
QY 304 GAATGGCAAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 363
DB 1026 GAATGGCAAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1085
QY 364 AACCATCTCCAAAGCCCAAGGCGCCCGGAGAACCAAGGTGTACACCTGCCCCATC 423
DB 1086 AACCATCTCCAAAGCCCAAGGCGCCCGGAGAACCAAGGTGTACACCTGCCCCATC 1145
QY 424 CCGGAGTGAAGTCAAGT 483
DB 1146 CCGGAGTGAAGTCAAGT 1205
QY 484 CAGCGATGTGCGGT 543
DB 1206 CAGCGATGTGCGGT 1265
QY 544 GCCTCCCGT 603
DB 1266 GCCTCCCGT 1325
QY 604 GAGCAGGT 663
DB 1326 GAGCAGGT 1385
QY 664 CCACTACAGCGAGAAAGAGCTTCTCTGTCTCTGCGGG 699
DB 1386 CCACTACAGCGAGAAAGAGCTTCTCTGTCTCTGCGGG 1421

RESULT 13
US-10-325-698-19
Sequence 19, Application US/10325698
Publication No. US2004007651A1
GENERAL INFORMATION:

APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/10/325,698
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/740,002
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 1428
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1425)
US-10-325-698-19

Query Match 90.4%; Score 694.4; DB 17; Length 1428;
Best Local Similarity 99.9%; Pred. No. 1.4e-171;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 AGCAGAGCCCAATCTTGTCACAAACTCACATGCCCACCTGCGCAGACCTGAAC 63
DB 726 AGCAGAGCCCAATCTTGTCACAAACTCACATGCCCACCTGCGCAGACCTGAAC 785
QY 64 CTTGGGGGGACCGTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 123
DB 786 CTTGGGGGGACCGTACGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 845
QY 124 CCGGACCCCTGAGGTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 183
DB 846 CCGGACCCCTGAGGTCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 905
QY 184 GTTCAACTGTGTCGT 243
DB 906 GTTCAACTGTGTCGT 965
QY 244 GCAGTACAAAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 303
DB 966 GCAGTACAAAGAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1025
QY 304 GAATGGCAAGAGTCAAGT 363
DB 1026 GAATGGCAAGAGTCAAGT 1085
QY 364 AACCATCTCCAAAGCCCAAGGCGCCCGGAGAACCAAGGTGTACACCTGCCCCATC 423
DB 1086 AACCATCTCCAAAGCCCAAGGCGCCCGGAGAACCAAGGTGTACACCTGCCCCATC 1145
QY 424 CCGGAGTGAAGTCAAGT 483
DB 1146 CCGGAGTGAAGTCAAGT 1205
QY 484 CAGCGATGTGCGGT 543
DB 1206 CAGCGATGTGCGGT 1265
QY 544 GCCTCCCGT 603
DB 1266 GCCTCCCGT 1325
QY 604 GAGCAGGT 663
DB 1326 GAGCAGGT 1385

Qy 664 CCACTACACGAGAGAGCCTCTCCCTGTCTCCGGG 699
 Db 1386 CCACTACACGAGAGAGCCTCTCCCTGTCTCCGGG 1421

RESULT 14

US-09-758-173-3
 ; Sequence 3, Application US/09758173
 ; Publication No. US20010024648A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/758,173

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teekin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ. ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1431 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1431

NAME/KEY: mat. peptide

LOCATION: 1..1431

US-09-758-173-3

Query Match 90.4%; Score 694.4; DB 9; Length 1431;
 Best Local Similarity 99.9%; Pred. No. 1.4e-171;
 Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AGCAGAGCCCAATCTTGTGCAAACTCAACATGCGCCACCGTCCAGACCTGAAT 63
 Db 729 AGCAGAGCCCAATCTTGTGCAAACTCAACATGCGCCACCGTCCAGACCTGAAT 788

Qy 64 CCGGGGGGAGCGTCACTTCTCCGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 123
 Db 789 CCGGGGGGAGCGTCACTTCTCCGCTCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 848

Qy 124 CCGAGACCCCTGAGGTCAATGCGGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 183
 Db 124 CCGAGACCCCTGAGGTCAATGCGGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 183

Db 849 CCGAGACCCCTGAGGTCAATGCGGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 908
 Qy 184 GTTCAACTGTGTAGTGGAGCGGCGTGGAGGTGATTAATGCCAAGAGAGAGAGAGAG 243
 Db 909 GTTCAACTGTGTAGTGGAGCGGCGTGGAGGTGATTAATGCCAAGAGAGAGAGAGAG 968
 Qy 244 GCAGTCAACAGCAGCAGTACCGGCTGTGACGCTCTCAACCGTCTGAGACAGAGAG 303
 Db 969 GCAGTCAACAGCAGCAGTACCGGCTGTGACGCTCTCAACCGTCTGAGACAGAGAG 1028
 Qy 304 GAATGGCAGAGAGTCAATGTCAGAGTCTTCAACAAAGCCCTCCAGCCCAATCGAG 363
 Db 1029 GAATGGCAGAGAGTCAATGTCAGAGTCTTCAACAAAGCCCTCCAGCCCAATCGAG 1088
 Qy 364 AACCATCTCCAAAGCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 423
 Db 1089 AACCATCTCCAAAGCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1148
 Qy 424 CCGGATGAGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
 Db 1149 CCGGATGAGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1208
 Qy 484 CAGCAGATGCGCTGTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
 Db 1209 CAGCAGATGCGCTGTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1268
 Qy 544 GCCTCCGCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 603
 Db 1269 GCCTCCGCTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1328
 Qy 604 GACAGGTGGCAGCAG 663
 Db 1329 GACAGGTGGCAGCAG 1388
 Qy 664 CCACTACACGAGAGAGAGCCTCTCCCTGTCTCCGGG 699
 Db 1389 CCACTACACGAGAGAGAGCCTCTCCCTGTCTCCGGG 1424

RESULT 15

US-09-758-173-11

; Sequence 11, Application US/09758173

; Publication No. US20010024648A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/758,173

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/383,916

FILING DATE:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teekin, Robin L.

```
/
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 012712-131
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-836-6620
/ TELEFAX: 703-836-2021
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1431 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: linear
/ MOLECULAR TYPE: peptide
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1431
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 1..1431
/
US-09-758-173-11

Query Match          90.4%; Score 694.4; DB 9; Length 1431;
Best Local Similarity 99.9%; Pred. No. 1.4e-171;
Matches 695; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCACATGCCACCGTGCACGACCTGAACT 63
DB 729 AGCAGAGCCCAATCTTGTGACAAACTCACATGCCACCGTGCACGACCTGAACT 788
QY 64 CTTGGGGGGGACCGTCACTCTTCTCTTCCCGGAAAAACCGAGACACCTCATGATTC 123
DB 789 CTTGGGGGGGACCGTCACTCTTCTCTTCCCGGAAAAACCGAGACACCTCATGATTC 848
QY 124 CCGGACCCCTGAGAGTCAATGCTGTGTGAGAGTGAAGCCAGAGACCCCTGAGGTCAA 183
DB 849 CCGGACCCCTGAGAGTCAATGCTGTGTGAGAGTGAAGCCAGAGACCCCTGAGGTCAA 908
QY 184 GTTCAACTGTGACGTGAGCGCGGTGAGAGTGCATTAATGCCAGACAAAGCCGCGGAGGA 243
DB 909 GTTCAACTGTGACGTGAGCGCGGTGAGAGTGCATTAATGCCAGACAAAGCCGCGGAGGA 968
QY 244 GCAGTCAACAGACGTAACCGGGTGTGACCGGTCTTCAACGCTCTGACACCGAGACTGGCT 303
DB 969 GCAGTCAACAGACGTAACCGGGTGTGACCGGTCTTCAACGCTCTGACACCGAGACTGGCT 1028
QY 304 GAATGGCAAGAGTACAGAGTCAAGGTCTTCAACAAAGCCCTCCAGCCCTCATCGAGAA 363
DB 1029 GAATGGCAAGAGTACAGAGTCAAGGTCTTCAACAAAGCCCTCCAGCCCTCATCGAGAA 1088
QY 364 AACCATCTCCAAAGCCAAAGGCGACGCCGAGAAACAAGGTGTACACCTGCCCCATC 423
DB 1089 AACCATCTCCAAAGCCAAAGGCGACGCCGAGAAACAAGGTGTACACCTGCCCCATC 1148
QY 424 CCGGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGTGTAAGGCTTCTATCC 483
DB 1149 CCGGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTGCTGTGTAAGGCTTCTATCC 1208
QY 484 CAGCGCATTCGCGGTGAGTGGAGAGCAATGGGACGCCGAGAACACTACAGAGCCAC 543
DB 1209 CAGCGCATTCGCGGTGAGTGGAGAGCAATGGGACGCCGAGAACACTACAGAGCCAC 1268
QY 544 GCTTCCCGTGTGATCTCGACGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAA 603
DB 1269 GCTTCCCGTGTGATCTCGACGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAA 1328
QY 604 GAGCAGGTGGCAGCAGGGGAAAGCTTTCATGCTCGTGAATGACATGAGGCTTGCACAA 663
DB 1329 GAGCAGGTGGCAGCAGGGGAAAGCTTTCATGCTCGTGAATGACATGAGGCTTGCACAA 1388
QY 664 CCACTACAGCAGAGAGGCTCTCCCTGTCTCCGG 639
DB 1389 CCACTACAGCAGAGAGGCTCTCCCTGTCTCCGG 1424
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Search completed: March 8, 2005, 09:11:54
Job time : 511 secs